

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Goli, Surya K.  
Hillman, Jennifer L.

(ii) TITLE OF THE INVENTION: A NOVEL GLUTATHIONE S-TRANSFERASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE GENOMICS, INC.  
(B) STREET: 3160 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: US  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/309,320  
(B) FILING DATE: May 11, 1999  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09 309,320  
(B) FILING DATE: May 11, 1999

(A) APPLICATION NUMBER: 09 096,571  
(B) FILING DATE: June 12, 1998

(A) APPLICATION NUMBER: 08 756,771  
(B) FILING DATE: November 26, 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE DOCKET NUMBER: PF 101 111

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415 855 0555  
(B) TELEFAX: 415-845-4166  
(C) TELEX:

(x) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(B) CLONE: Consensus

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| ATGGGATGCAA | GGGCGAAGCT  | CGACTATGCT | AAAGGAAACG | GGGCGAATGA | TCGCTGCAAA  | 7   |
| TGGGTTTAG   | CTGGCGCGCG  | AGTCGAGTTT | GATGAAGAAT | TTCTGCAAA  | AAAAGAACAG  | 12  |
| TTGTACAAGT  | TGCAGGATGG  | TAACCACTG  | CTGTTCCAAC | AAGTGGCCAT | GTTTGAAATT  | 180 |
| GACGGGATGA  | AGTTGGGTACA | GACCGGAAGC | ATTCTCGACT | ACATACGAGA | CAAGCACAAAT | 240 |
| CTCTTTGGCA  | AGAACCTCAA  | GGAGAGAACC | CTGATTGACA | TGTACCTGGA | GGGACACTG   | 300 |
| GATCTCTTG   | AACTGCTTAT  | CATCGATCTT | CTTTAAAAAC | CAGATGATGA | CAAAAAAGAA  | 360 |
| CTGCTTAAAG  | GGGCGAAG    | GGTAAATAT  | ATATACCTTC | CTGCTTGA   | AAAGATTTTA  | 420 |
| AGGGCTTACG  | GAAAAAGCTT  | TCTGTTCCT  | ATTCAGCTCA | GGGCTTGA   | TTGTATTTTA  | 480 |

TACAGTCATG TTTTAATGGA TCCCAGCTCT GTCATGGTGC TATCTATGTA TTAAGTTGGG  
TCCCTAAGTTG GGTCTTTTGT

780  
800

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Ger.Bank
- (B) CLONE: 825605

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Lys | Pro | Lys | Leu | His | Tyr | Ser | Asn | Thr | Arg | Gly | Arg | Met | 1   | 5   | 10  | 15  |
| Glu | Ser | Ile | Arg | Trp | Leu | Leu | Ala | Ala | Ala | Gly | Val | Glu | Phe | Glu | Glu | 20  | 25  | 30  |     |
| Lys | Phe | Ile | Lys | Ser | Ala | Glu | Asp | Leu | Asp | Lys | Leu | Arg | Asn | Asp | Gly | 35  | 40  | 45  |     |
| Tyr | Leu | Met | Phe | Gln | Gln | Val | Pro | Met | Val | Glu | Ile | Asp | Gly | Met | Lys | 50  | 55  | 60  |     |
| Leu | Val | Gln | Thr | Arg | Ala | Ile | Leu | Asn | Tyr | Ile | Ala | Ser | Lys | Tyr | Asn | 65  | 70  | 75  | 80  |
| Leu | Tyr | Gly | Lys | Asp | Ile | Lys | Glu | Lys | Ala | Leu | Ile | Asp | Met | Tyr | Ile | 85  | 90  | 95  |     |
| Glu | Gly | Ile | Ala | Asp | Leu | Gly | Glu | Met | Ile | Leu | Leu | Leu | Pro | Phe | Thr | 100 | 105 | 110 |     |
| Gln | Pro | Glu | Gln | Asp | Ala | Lys | Leu | Ala | Leu | Ile | Gln | Glu | Lys | Thr |     | 115 | 120 | 125 |     |
| Lys | Asn | Arg | Tyr | Phe | Pro | Ala | Phe | Glu | Lys | Val | Leu | Lys | Ser | His | Gly | 130 | 135 | 140 |     |
| Gln | Asp | Tyr | Leu | Val | Gly | Asn | Lys | Leu | Ser | Arg | Ala | Asp | Ile | His | Leu | 145 | 150 | 155 | 160 |
| Val | Glu | Leu | Leu | Tyr | Tyr | Val | Glu | Glu | Leu | Asp | Ser | Ser | Leu | Ile | Ser | 165 | 170 | 175 |     |
| Ser | Phe | Pro | Leu | Leu | Lys | Ala | Leu | Lys | Thr | Arg | Ile | Ser | Asn | Leu | Pro | 180 | 185 | 190 |     |
| Thr | Val | Lys | Lys | Phe | Leu | Gln | Pro | Gly | Ser | Pro | Arg | Lys | Pro | Pro | Met | 195 | 200 | 205 |     |
| Asp | Glu | Lys | Ser | Leu | Glu | Glu | Ser | Arg | Lys | Ile | Phe | Arg | Phe |     |     | 210 | 215 | 220 |     |

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 159141

```

      1           5           10           15
Glu Ser Thr Arg Trp Leu Leu Ala Ala Ala Gly Val Glu Phe Glu Glu
      20           25           30
Lys Phe Ile Lys Ser Ala Glu Asp Leu Asp Lys Leu Arg Asn Asp Gly
      35           40           45
Tyr Leu Met Phe Gln Gln Val Pro Met Val Glu Ile Asp Gly Met Lys
      50           55           60
Leu Val Gln Thr Arg Ala Ile Leu Asn Tyr Ile Ala Ser Lys Tyr Asn
      65           70           75           80
Leu Tyr Gly Lys Asp Ile Lys Glu Arg Ala Leu Ile Asp Met Tyr Ile
      85           90           95
Glu Gly Ile Ala Asp Leu Gly Glu Met Ile Leu Leu Leu Pro Val Cys
      100           105           110
Pro Pro Glu Glu Lys Asp Ala Lys Leu Ala Leu Ile Lys Glu Lys Ile
      115           120           125
Lys Asn Arg Tyr Phe Pro Ala Phe Glu Lys Val Leu Lys Ser His Gly
      130           135           140
Gln Asp Tyr Leu Val Gly Asn Lys Leu Ser Arg Ala Asp Ile His Leu
      145           150           155           160
Val Glu Leu Leu Tyr Tyr Val Glu Glu Leu Asp Ser Ser Leu Ile Ser
      165           170           175           180
Ser Phe Pro Leu Leu Lys Ala Leu Lys Thr Arg Ile Ser Asn Leu Pro
      185           190           195
Thr Val Lys Lys Phe Leu Gln Pro Gly Ser Pro Arg Lys Pro Pro Met
      200           205           210
Asp Glu Lys Ser Leu Glu Glu Ala Arg Lys Ile Phe Arg Phe
      215           220

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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (E) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 193710

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Ala Ala Lys Pro Lys Leu Tyr Tyr Phe Asn Gly Arg Gly Arg Met
  1           5           10           15
Glu Ser Ile Arg Trp Leu Leu Ala Ala Ala Gly Val Glu Phe Glu Glu
      20           25           30
Gln Phe Ile Gln Thr Arg Gln Gln Tyr Gln Lys Met Gln Lys Asp Gly
      35           40           45
His Leu Leu Phe Gly Gln Thr Phe Leu Val Gln Ile Arg Gly Met Met
      50           55           60
Leu Thr Gln Thr Arg Ala Ile Leu Ser Tyr Leu Ala Ala Lys Tyr Asn
      65           70           75           80
Leu Tyr Gly Lys Asp Leu Lys Glu Arg Val Arg Ile Asp Met Tyr Ala
      85           90           95
Asp Gly Thr Gln Asp Leu Met Met Met Ile Ala Val Ala Pro Phe Lys
      100           105           110
Thr Pro Lys Gln Lys Gln Gln Ser Tyr Asp Leu Ile Leu Asp Arg Ala
      115           120           125

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PF 0161 & DIV

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |     |     |     |
| Leu | Glu | Ala | Ile | Leu | Met | Val | Glu | Glu | Leu | Ser | Ala | Pro | Val | Leu | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Phe | Pro | Leu | Leu | Gln | Ala | Phe | Lys | Thr | Arg | Ile | Ser | Asn | Ile | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Thr | Ile | Lys | Lys | Phe | Leu | Gln | Pro | Gly | Ser | Gln | Arg | Lys | Pro | Pro | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Gly | Pro | Tyr | Val | Glu | Val | Val | Arg | Ile | Val | Leu | Lys | Phe |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |